

Genome version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 15, 2003, 15:39:12, Search time 7.28571 seconds  
(without alignments)  
28.464 Million cell updates/sec

Title: US-09-856-070-18

Perfect score: 24  
Sequence: 1 KEELM 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	95	GVPS_BACME	G68671 bacillus me
2	24	100.0	174	RL10_HELPJ	G2K32 helicobacte
3	24	100.0	164	RL10_HELPJ	P56036 helicobacte
4	24	100.0	165	DEST_CHICK	P18359 gallus gall
5	24	100.0	165	DEST_HUMAN	P18202 homo sapien
6	24	100.0	165	DEST_MOUSE	G30055 mus musculu
7	24	100.0	167	CAPR_ATRNU	P41210 atriplex nu
8	24	100.0	168	VA34_VACCV	P1057 vaccinia vi
9	24	100.0	168	VA34_VACCV	P24761 vaccinia vi
10	24	100.0	168	VA34_VACCV	P30851 variola vir
11	24	100.0	283	APMG_HRWCH	P26211 crinia chr
12	24	100.0	291	CV3A_MOUSEP	P46737 mus musculu
13	24	100.0	312	IGF2_PAT	P55215 rattus norv
14	24	100.0	316	Y014_HUMAN	P46736 homo sapien
15	24	100.0	316	Y014_MPTTA	G60349 methanococ
16	24	100.0	330	GAPP_SULAC	P39464 sulfolobus
17	24	100.0	434	CHPH_BOVIN	P04806 bos taurus
18	24	100.0	435	ICP2_MOUSEP	P24544 mus musculu
19	24	100.0	436	COM2_ARCHB	G29531 arabidopsi
20	24	100.0	448	KIM2_HUMAN	G4532 homo sapien
21	24	100.0	467	KIM6_HUMAN	G76013 homo sapien
22	24	100.0	476	GBPH_HUMAN	P16870 homo sapien
23	24	100.0	476	CHPH_MOUSEP	G00493 mus musculu
24	24	100.0	476	CHPH_RAT	P15087 rattus norv
25	24	100.0	492	TIG_RH110	G28168 rhizobium l
26	24	100.0	496	ML15_APATH	G00580 arabidopsi
27	24	100.0	526	IEG3_HSV7J	P52355 human herpe
28	24	100.0	526	ML11_APATH	G47621 arabidopsi
29	24	100.0	561	NCAP_P1ARV	P03541 pichinde ar
30	24	100.0	576	MOHS_HUMAN	P26008 homo sapien
31	24	100.0	576	MOHS_MOUSEP	P26041 mus musculu
32	24	100.0	576	MOHS_PIG	P26042 sus scrofa
33	24	100.0	580	EZRI_BOVIN	P31976 bos taurus

34	24	100.0	583	1	RADI_HUMAN	P45241 homo sapien
35	24	100.0	583	1	RADI_MOUSE	P26043 mus musculu
36	24	100.0	583	1	PAC1_PIG	P56044 sus scrofa
37	24	100.0	585	1	EZRI_HUMAN	P15311 homo sapien
38	24	100.0	585	1	EZRI_MOUSE	P26040 mus musculu
39	24	100.0	596	1	MOHS_HUMAN	G00557 homo sapien
40	24	100.0	601	1	GLMS_PYRAE	G02120 p glucosami
41	24	100.0	635	1	F3SIL_TREPA	G83746 trepanula p
42	24	100.0	647	1	KNRI_DROMO	P13054 drosophila
43	24	100.0	676	1	DNLJ_HACST	G07703 bacillus st
44	24	100.0	721	1	DNAK_APHHA	G52960 aphanothece
45	24	100.0	868	1	AC02_SYNT3	P74582 synchocyst

## ALIGNMENTS

RESULT 1			
ID	GVPS_BACME	STANDARD:	PPT: 95 AA.
AC	O68671;		
DI	15 JUN 2002 (Rel. 41, Created)		
DI	15 JUN 2002 (Rel. 41, Last sequence update)		
DI	15 JUN 2002 (Rel. 41, Last annotation update)		
DE	Gas vesicle protein GvpS.		
GN	GVPS.		
OS	Bacillus megaterium.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_taxonomy:1404;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STEIN-VI1560;		
KA	Medline:98233742; PubMed:9573198;		
KA	Li N., Cannon M.C.;		
KT	"Gas vesicle genes identified in Bacillus megaterium and functional expression in Escherichia coli.";		
PL	J. Bacteriol. 180:2450-2458(1998).		
CC	-!- SIMILARITY: BELONGS TO THE GAS VESICLE PROTEIN TYPE A FAMILY.		
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CC	EMBL: AF053765; AAC38410.1;		
DR	InterPro, Ipp060638; Gas_vesicle		
DR	Pfam: PF00741; Gas_vesicle; 1.		
DR	Trdbm, P060638; Gas_vesicle; 1.		
DR	PROSITE, P50024; GAS_VESICLE_A.1; FALSE_NEG.		
DR	PROSITE, P50069; GAS_VESICLE_A.2; FALSE_NEG.		
KW	Gas vesicle.		
SQ	SEQUENCE 95 AA: 10422 MW: 10422 MW: AAFVAFV2725603B CR064;		

Query Match						
Best local similarity 100.0%, Score 24, DB 1, Length 95;						
Matches 5, Conservative 6, Mismatches 0, Gaps 0;						
QY	1 KEELM 5					
DB	76 KEELM 80					
RESULT 2						
RL10_HELPJ	STANDARD;	PRT;	164 AA.			
DI 30 MAY 2000 (Rel. 39, Created)						
DI 30 MAY 2000 (Rel. 39, Last sequence update)						
DI 16 OCT 2001 (Rel. 40, Last annotation update)						
DE 50S ribosomal protein L10.						

GN RPL1 OR JHE1123.  
 OS Helicobacter pylori 399 (Campylobacter pylori 399).  
 CC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 CC Helicobacter  
 CC NCHI\_TaxID=85963;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99120557; PubMed 9923682;  
 RA Alm R.A., Ling D.-S.L., Moir D.L., King R.L., Brown E.D., Dorig P.C.,  
 RA Smith D.R., Noonan R., Cullis R.C., deJonghe R.L., Carmel G.,  
 RA Lumino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
 RA Gibson R., Morberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori.";  
 RL Nature 397:176-180(1999).  
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
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EMBL: AF001540; AA006701.1;  
 DR InterPro: IPR001790; Ribosomal\_L10.  
 DR InterPro: IPR002363; Ribosomal\_L10eub.  
 DR Pfam: PF00466; Ribosomal\_L10; 1.  
 DR PROSITE: PS01109; RIBOSOMAL\_L10; 1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 164 AA; 18573 MW; F307C2448H5F17F6 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 DB 132 KEELM 136

RESULT 3  
 ID R10\_HELPY STANDARD; PRT; 164 AA.  
 AC P56036;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein l10.  
 GN RPL1 OR HPI200.  
 OS Helicobacter pylori (Campylobacter pylori).  
 CC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 CC Helicobacter.  
 CC NCHI\_TaxID=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=26695 / AF00 700392;  
 RX MEDLINE=97494467; PubMed 9252185;  
 RA Tomb J.F., White O., Kiehlavag A.R., Klek H.-P., Gill S., Dougherty B.A.,  
 RA Fleischmann R.D., Ketchum K.A., Zhou L., Kirkness E.F., Peterson S.,  
 RA Loftus B., Richardson D., Dodson R., Khatak H.G., Glodek A.,  
 RA McKenney K., FitzGerald L.M., Ito N., Adams M.D., Hickey E.K.,  
 RA Berg D.E., Gacyayre T.B., Unterbach T.E., Peterson J.D., Kelley J.M.,  
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,  
 RA Hayes W.S., Borodovsky M., Karp P.B., Smith H.O., Fraser C.M.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the gastric pathogen Helicobacter  
 RT pylori.";  
 RL Nature 398:539-547(1997).  
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

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EMBL: AF000626; AA008246.1;  
 DR TIGR: HPI200;  
 DR InterPro: IPR001790; Ribosomal\_L10.  
 DR InterPro: IPR002363; Ribosomal\_L10eub.  
 DR Pfam: PF00466; Ribosomal\_L10; 1.  
 DR PROSITE: PS01109; RIBOSOMAL\_L10; 1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 164 AA; 18605 MW; 9915415p78AF5D97 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 DB 132 KEELM 136

## RESULT 4

ID DEST\_CHICK STANDARD; PRT; 165 AA.  
 AC PIR359;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Destrin (Actin-depolymerizing factor) (ADP).  
 GN DSTN OR DSN.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC NCHI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 101-111 AND 116-134.  
 RC TISSUE=Brain;  
 RX MEDLINE=91027754; PubMed 2221773;  
 RA Adams M.E., Minamide L.S., Duester G., Hamburg J.R.;  
 RT "Nucleotide sequence and expression of a cDNA encoding chick brain  
 RT actin depolymerizing factor.";  
 RL Biochemistry 29:7434-7439(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=91027755; PubMed 1699599;  
 RA Abe H., Endo T., Yamamoto K., Ohinata T.;  
 RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin  
 RT actin-regulatory proteins exhibit high structural homology.";  
 RL Biochemistry 29:7420-7425(1990).  
 CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-  
 CC ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-  
 CC INDEPENDENT MANNER.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS AND FAMILY.

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EMBL: J02912; AAA48575.1;  
 EMBL: M55660; AAA48573.1;

DR PIR: A35702; A35702.  
 DR PIR: A35703; A35703.  
 DR HSP: P18282; 1AK6.  
 DR InterPro: IPR002108; Actbind\_cofin.  
 DR Pfam: PF00241; cofilin\_ADF\_1.  
 DR PRINTS: PR00006; COFILIN.  
 DR ProDom: PD002129; Actbind\_cofin; 1.  
 DR SMART: SM00102; ADF; 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.  
 KW Actin-binding.  
 FT DOMAIN 30 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).  
 SQ SEQUENCE 165 AA; 18422 MW; 709920024514659 GC%;

Query Match 100.0%, Score 24, DB 1, Length 165.  
 Best Local Similarity: 100.0%, Pred. No. 54.  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KEELM 5  
 DB 96 KEELM 100

RESULT 5

DEST_HUMAN	STANDARD:	PRT:	165 AA:
AC P18282;			
DT 01-NOV-1990 (Ref. 16, Created)			
DT 01-NOV-1990 (Ref. 16, Last sequence update)			
DT 15-JUN-2002 (Ref. 41, Last annotation update)			
DE Desitin (Actin-depolymerizing factor) (ADF).			
CN DSTN OR DSN OR ACTDP.			
OS Homo sapiens (Human), and			
OS Sus scrofa (Pig).			
OC Eukaryota, Metazoa, Chordata, Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria, Primates; Carnivora, Hominoidea, Homo.			
OX NCBI_TaxID=9606, 9823;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC SPECIES-Human; TISSUE-Brain;			
RX MEDLINE=9400200q; PubMed=8369167;			
RA Hawkins M., Pope B., Maciver S. K., Woods A. G.			
RT "Human actin depolymerizing factor mediates a pH-sensitive			
RL destruction of actin filaments."			
RN Biochemistry 32:9085-9092(1993)			
RP SEQUENCE FROM N.A.			
RC SPECIES-Human;			
RX MEDLINE=21638749; PubMed=11780052.			
RA Deloukas P., Matthews L.H., Ashurst J., Barton J., Gilbert J.G.R.,			
RA Jones M., Starikov G., Almeida J.P., Babington A.K., Bagdikian C.L.,			
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA Beasley G.P., Bird C.F., Blake S.E., Bridgman A.M., Brown A.J.,			
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA Coulson A., Coville G.T., Deadman P., Dhami P.D., Dunn M.,			
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam P., Hall P.E.,			
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J., Howden P.J.,			
RA Huckle E., Hunter A.R., Hunt S.E., Jekoski K., Johnson C.M., Johnson D.,			
RA Kay M.P., Kimberley A.M., King A., Knight A., Laird G.K., Lawlor S.,			
RA Lehtavirta M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.T.D.,			
RA Marsh V.L., Martin S.L., McConachie I.T., Melay C., McMurray A.A.,			
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,			
RA Phillimore R.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA Rice C.M., Ross M.T., Scott C.F., Shih H.K., Showkhan P., Sims S.,			
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA Tracey A., Tromas A.C., Vaudin M., Wall M., Wallis T.M.,			
RA Whitehead S.L., Whitaker P., Willey D.L., Williams C., Williams S.A.,			
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			

Rogers J.;  
 "The DNA sequence and comparative analysis of human chromosome 20";  
 Nature 414 865-87(2001).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-Human; TISSUE-lung;  
 RA Strausberg R.;  
 RI Submitted (JUN 2001) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.; AND SEQUENCE OF 53-69 AND 96-112.  
 RC SPECIES-Pig; TISSUE-Brain;  
 RX MEDLINE=96202824; PubMed=215828;  
 RA Moriyama K., Nishida F., Yamazawa N., Sakai H., Matsumoto S.,  
 RA Iida K., Yahara I.;  
 ET "Desitin, a mammalian actin depolymerizing protein, is closely  
 related to cofilin. Cloning and expression of porcine brain desitin  
 cDNA";  
 RI J. Biol. Chem. 265:5768-5773(1990).  
 RN [5]  
 RN STRUCTURE BY NMR.  
 RP SPECIES-Pig;  
 RX MEDLINE=96270507; PubMed=8674111;  
 RA Hatanaka H., Ogura K., Moriyama K., Ichikawa S., Yahara I.,  
 RA Inagaki F.;  
 RT "Tertiary structure of desitin and structural similarity between two  
 actin-regulating protein families";  
 RI Cell 85:1047-1055(1996).  
 CC -!- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-  
 ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-  
 INDEPENDENT MANNER.  
 CC -!- ISSUE SPECIFICITY: WIDELY DISTRIBUTED IN VARIOUS TISSUES.  
 CC -!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
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DR EMBL: S65738; AAB29361.1; -;  
 DR EMBL: AL142765; CAC10545.1; -;  
 DR EMBL: WC009477; AAH09477.1; -;  
 DR EMBL: S60953; BAA14105.1; -;  
 DR PIR: A35179; A35179.  
 DR PIR: A54184; A54184.  
 DR PDB: 1AK6; 12-NOV-97.  
 DR PDB: 1AK7; 15-OCT-97.  
 DR Genbank: U00015750; DSTN.  
 DR InterPro: IPR002108; Actbind\_cofin.  
 DR Pfam: PF00241; cofilin\_ADF\_1.  
 DR PRINTS: PR00006; COFILIN.  
 DR ProDom: PD002129; Actbind\_cofin; 1.  
 DR SMART: SM00102; ADF; 1.  
 DR PROSITE: PS00325; ACTIN\_DEPOLYMERIZING; 1.  
 KW Actin-binding; 3D-structure.  
 FT DOMAIN 30 34  
 FT DOMAIN 106 125 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 SQ SEQUENCE 165 AA; 18506 MW; 89684157924100E GC%;

Query Match 100.0%, Score 24, DB 1, Length 165.  
 Best Local Similarity: 100.0%, Pred. No. 54.  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KEELM 5  
 DB 96 KEELM 100

RESULT 6

DEST_MOUSE	STANDARD:	PRT:	165 AA:
AC P18282;			
DT 01-NOV-1990 (Ref. 16, Created)			
DT 01-NOV-1990 (Ref. 16, Last sequence update)			
DT 15-JUN-2002 (Ref. 41, Last annotation update)			
DE Desitin (Actin-depolymerizing factor) (ADF).			
CN DSTN OR DSN OR ACTDP.			
OS Homo sapiens (Human), and			
OS Sus scrofa (Pig).			
OC Eukaryota, Metazoa, Chordata, Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria, Primates; Carnivora, Hominoidea, Homo.			
OX NCBI_TaxID=9606, 9823;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC SPECIES-Human; TISSUE-Brain;			
RX MEDLINE=9400200q; PubMed=8369167;			
RA Hawkins M., Pope B., Maciver S. K., Woods A. G.			
RT "Human actin depolymerizing factor mediates a pH-sensitive			
RL destruction of actin filaments."			
RN Biochemistry 32:9085-9092(1993)			
RP SEQUENCE FROM N.A.			
RC SPECIES-Human;			
RX MEDLINE=21638749; PubMed=11780052.			
RA Deloukas P., Matthews L.H., Ashurst J., Barton J., Gilbert J.G.R.,			
RA Jones M., Starikov G., Almeida J.P., Babington A.K., Bagdikian C.L.,			
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA Beasley G.P., Bird C.F., Blake S.E., Bridgman A.M., Brown A.J.,			
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA Coulson A., Coville G.T., Deadman P., Dhami P.D., Dunn M.,			
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam P., Hall P.E.,			
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J., Howden P.J.,			
RA Huckle E., Hunter A.R., Hunt S.E., Jekoski K., Johnson C.M., Johnson D.,			
RA Kay M.P., Kimberley A.M., King A., Knight A., Laird G.K., Lawlor S.,			
RA Lehtavirta M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.T.D.,			
RA Marsh V.L., Martin S.L., McConachie I.T., Melay C., McMurray A.A.,			
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.L.,			
RA Phillimore R.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA Rice C.M., Ross M.T., Scott C.F., Shih H.K., Showkhan P., Sims S.,			
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA Tracey A., Tromas A.C., Vaudin M., Wall M., Wallis T.M.,			
RA Whitehead S.L., Whitaker P., Willey D.L., Williams C., Williams S.A.,			
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			

CC G90095;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Desirin (Actin-depolymerizing factor) (ADF).  
 GN DESIN OR DSN OR SD23.  
 OS MUS MUSCULUS (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Saki N., Hattori A., Kozuma S., Muramatsu M., Saito T.;  
 RI "Mouse actin depolymerizing factor sld23";  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS (F-  
 ACTIN) AND BINDS TO ACTIN MONOMERS (G-ACTIN). ACTS IN A PH-  
 INDEPENDENT MANNER.  
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
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 CC  
 CC EMBL; AR025406; BAA84691.1;  
 DR HSSP; P18282; IAK6  
 DR MGI; MGI:1924270; Dstn.  
 DR InterPro; IPR002108; Actbind\_cofin.  
 DR Pfam; PF00241; coillin\_ADF; 1.  
 DR PRINTS; PR00066; COFILIN.  
 DR ProDom; PD002129; Actbind\_cofin; 1.  
 DR SMART; SM00102; ADF; 1.  
 DR PROSITE; PS00125; ACTIN\_DEPOLYMERIZING; 1.  
 KW Actin-binding.  
 FT DOMAIN 40 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 106 125 ACTIN-BINDING (POTENTIAL).  
 SQ SEQUENCE 165 AA; 18521 MW; 42R007647693667 CP\*64;  
 Query Match 100.0%; Score 24; DH 1; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KEELM 5  
 DB 96 KEELM 100  
 RESULT 7  
 CATR\_ATRNU STANDARD; PRT; 167 AA.  
 ID CATR\_ATRNU  
 AV P41210;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 41, Last sequence update)  
 DT 01-NOV-1995 (Rel. 42, Last annotation update)  
 DE Caltractin (centrin).  
 OS Atriplex nummularia.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllaceae; Gnocpodiales; Atriplex.  
 CC NCBI\_TaxID=4554;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhu J. K., Brossan R.A., Hasegawa P.M.;  
 RI "An Atriplex nummularia cDNA with sequence relatedness to the algal  
 RI caltractin gene".  
 RL Plant Physiol. 99:1744-1745(1992).  
 CC -1- FUNCTION: PLAYS A FUNDAMENTAL ROLE IN MICROTUBULE-ORGANIZING  
 CC CENTER STRUCTURE AND FUNCTION.  
 CC -1- SUBCELLULAR LOCATION: CYTOSOL; SOME OF INTERPHASE AND MITOTIC CELLS.

CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BELONGS  
 CC THE CALTRACTIN/CDC31 SUBFAMILY.  
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 CC  
 CC EMBL; M90970; ?; NOT\_ANNOTATED\_CDS.  
 DR HSSP; P02593; ICDM.  
 DR InterPro; IPR002048; EF-hand.  
 DR Pfam; PF00036; efhand; 4.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR SMART; SM00054; EFH; 4.  
 DR PROSITE; PS00018; EF\_HAND; 4.  
 KW Calcium-binding; Repeat; Cell division; Mitosis.  
 FT CA-BIND 35 46 EF-HAND 1 (PROBABLE).  
 FT CA-BIND 71 82 EF-HAND 2 (PROBABLE).  
 FT CA-BIND 108 119 EF-HAND 3 (PROBABLE).  
 FT CA-BIND 144 155 EF-HAND 4 (PROBABLE).  
 SQ SEQUENCE 167 AA; 19244 MW; 3A2D0AC6956HRD6C CRC64;  
 Query Match 100.0%; Score 24; DH 1; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KEELM 5  
 DB 97 KEELM 101  
 RESULT 8  
 VA34\_VACCC STANDARD; PRT; 168 AA.  
 ID VA34\_VACCC  
 AC P21057;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein A34.  
 GN A34.  
 OS Vaccinia virus (strain Copenhagen).  
 CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 CC Orthopoxvirus.  
 CC NCBI\_TaxID=10249;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-9101027; PubMed-2219722;  
 RA Goebel S T., Johnson G P., Perkus M.E., Davis S.W., Winslow J.P.,  
 RA Paoletti E.;  
 RT "The complete DNA sequence of vaccinia virus.";  
 RL Virology 179:247-266(1990).  
 RN [2]  
 RP COMPLETE GENOME.  
 RA Goebel S T., Johnson G P., Perkus M.E., Davis S.W., Winslow J.P.,  
 RA Paoletti E.;  
 RT "Appendix to 'The complete DNA sequence of vaccinia virus.'";  
 RL Virology 179:517-563(1990).  
 CC -1- FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED  
 CC VIRUS AND GRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.  
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 CC  
 CC EMBL; M15027; AAA48161.1;  
 DR HSSP; 14520; 14520.

DR InterPro: IPR001304; Lectin\_C.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Transmembrane.  
 FT TRANSMEM 1 20 SIGNAL-ANCHOR.  
 FT DOMAIN 21 168 EXTRACELLULAR  
 SQ SEQUENCE 168 AA: 19555 MW: 37028480.140255 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 DB 39 KEELM 43

## RESULT 9

VA34\_VACCV STANDARD; PRT; 168 AA.  
 AC P24761:  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE Protein A34.  
 GN A34R OR SALIAR.  
 OS Vaccinia virus (strain WR).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus  
 OX NCBI\_TaxID=10254;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91259083; PubMed=2045793;  
 RA Smith G.L., Chan Y.S., Howard S.T.,  
 RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WP from near  
 the right inverted terminal repeat.";  
 PL J. Gen. Virol. 72:1349-1376(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91310644; PubMed=1856205;  
 RA Areqadzi A.R.Y., Abn R.Y., Moss B.,  
 RT "Identification, sequence, and expression of the gene encoding a Mr  
 35,030 subunit of the vaccinia virus DNA-dependent RNA polymerase.";  
 PL J. Biol. Chem. 266:13712-13718(1991).  
 CC -1- FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED  
 CC VIRUS AND EGRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.  
 CC  
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EMBL: D11079, BAA01804.1;  
 EMBL: M61187, AAA48331.1;  
 EMBL: A19583, CAA01480.1;  
 DR PIR: T01770, T01770  
 DR InterPro: IPR001304; Lectin\_C  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Transmembrane.  
 FT TRANSMEM 1 20 SIGNAL-ANCHOR.  
 FT DOMAIN 21 168 EXTRACELLULAR  
 SQ SEQUENCE 168 AA: 19555 MW: 69F72EA9D971F19F CRC64;

Query Match 100.0%; Score 24; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 DB 39 KEELM 43

## RESULT 10

VA34\_VAFV STANDARD; PRT; 168 AA.  
 AC P33851;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Protein A34.  
 GN A34R OR A37R.  
 OS Variola virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus  
 OX NCBI\_TaxID=10255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=India-1967 / Isolate Ind3;  
 RX MEDLINE=92209372; PubMed=1666548;  
 RA Shechukunov S.N., Matyunikova S.S., Iotchenko A.V., Blinov V.M.,  
 FA Chichikov V.E., Gubarev V.V., Safonov P.F., Rodnyakov S.B.,  
 FA Shechukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakchiev L.S.;  
 RT "Creation of a clone library of fragments from the natural variola  
 RT virus and study of the structural and functional organization of  
 RT viral genes from a circle of hosts.";  
 PL Dokl. Akad. Nauk SSSR 421:402-406(1991)  
 RN [2]  
 RP COMPLETE GENOME.  
 RX STRAIN=India-1967 / Isolate Ind3;  
 RX MEDLINE=9320281; PubMed=8384129;  
 RA Shechukunov S.N., Blinov V.M., Sandakchiev L.S.;  
 RT "Genes of variola and vaccinia viruses necessary to overcome the host  
 RT protective mechanisms.";  
 RL FEBS Lett. 319:80-83(1993).

-1- FUNCTION: REQUIRED FOR THE ENVELOPMENT OF INTRACELLULAR NAKED  
 CC VIRUS AND EGRESS OF EXTRACELLULAR ENVELOPED VIRUS FROM THE CELL.  
 CC (BY SIMILARITY).

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EMBL: X64198, CAA49082.1;  
 EMBL: X61115, CAA47508.1;  
 DR PIR: P35852; B36952.  
 DR PIR: S46864; S46864.  
 DR InterPro: IPR001304; Lectin\_C  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Transmembrane.  
 FT TRANSMEM 1 20 SIGNAL-ANCHOR.  
 FT DOMAIN 21 168 EXTRACELLULAR.  
 SQ SEQUENCE 168 AA: 19611 MW: 28EABFD95FA09634 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 DB 39 KEELM 43

RESULT 11  
 ARBG\_ERWCH

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ID ARBO_PFWCH STANDARD: PRT: 283 AA.
AC P26211;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE beta-glucoside operon antiterminator.
GN ARBO.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID-556;
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE-92121114; PubMed-1733212;
RA el Hassouni M., Benissat B., Chippaux M., Barras F.;
RT "Nucleotide sequences of the arb genes, which control beta-glucoside
RT utilization in Erwinia chrysanthemi, compared with the Escherichia
RT coli ba operon and evidence for a new beta-glycosylase family
RT including enzymes from eubacteria, archaeobacteria, and humans."
RL J. Bacteriol. 174:765-777(1992).
CC -!- FUNCTION: MEDIATES THE POSITIVE REGULATION OF THE BETA-GLUCOSIDE
CC (ARB) OPERON BY FUNCTIONING AS A TRANSCRIPTIONAL ANTITERMINATOR
CC THIS IS A RNA-RIBING PROTEIN THAT RECOGNIZES A SPECIFIC SEQUENCE
CC LOCATED JUST UPSTREAM OF TWO TERMINATION SITES WITHIN THE OPERON
CC (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED AND INACTIVATED BY ARRF (11-HG1). THE DEGREE
CC OF PHOSPHORYLATION IS DEPENDENT ON THE PRESENCE OR ABSENCE OF
CC BETA-GLUCOSIDES WHICH ACT AS INDUCERS OF THE OPERON EXPRESSION.
CC ADDITION OF INDUCER RESULT IN THE RAPID DEPHOSPHORYLATION OF ARRG
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TRANSCRIPTIONAL ANTITERMINATOR HCIG
CC FAMILY.
CC -----
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CC -----
DR EMBL: M41772; AAA24813.1; -
DR PIR: A42603; A42603
DR RSP: P15401; 1A0U
DR InterPro: IPR001550; BglG_antitermin.
DR Pfam: PF00874; BglG_antitermin; 2.
DR Pfam: PF03123; CAT_RBD; 1.
DR PROSITE: PS00654; ANTITERMINATORS_HGIG; 1.
KW Transcription regulation. Activator. RNA binding. Phosphorylation.
SQ SEQUENCE 283 AA; 33620 MW; A58VADRGGRN1IA4K RPO64;

Query Match 100.0%; Score 24; DB 1; Length 283;
Best local Similarity 100.0%; Pred. No. 93.
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
Db 260 KEELM 264
|||||

RESULT 12
C61A_MOUSE STANDARD: PRT: 291 AA.
AC P46737; Q9D025;
DT 01-NOV-1995 (Rel. 12, Created)
DT 01-NOV-1995 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C6.1A protein.
GN C6.1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muteicostomia;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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OX NCBI_TaxID-10090;
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE-94067776; PubMed-8247530;
RA Fisch P., Forster A., Sherrington P.D., Oyer M.J.S., Rabbitts T.H.;
RT "The chromosomal translocation t(X;14)(q28;q11) in T-cell pro-
RT lymphocytic leukaemia breaks within one gene and activates another."
RL Oncogene 8:3271-3276(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6J; TISSUE-Embryo;
RX MEDLINE-21085660; PubMed 11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Adachi T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasakawa I., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King H., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole C., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bolunda N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nerdes P., Ping B., Pinwald M., Podríguez L., Sakamoto N.,
RA Sasaki H., Salo K., Schoenbach C., Seya T., Shibata Y., Storch K.-E.,
RA Suzuki H., Toyochika K., Watz K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Horris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE-Breast tumor;
RA Strausberg R.;
RV Submitted (JAN-2002) to the FMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PSMD7/C6.1A FAMILY.
CC -----
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CC -----
DR EMBL: S68022; AAB29006.2; -
DR EMBL: AK011876; BAB27894.1; -
DR EMBL: BC021313; AAH21313.1; -
DR InterPro: IPR000555; Mov34.
DR Pfam: PF01398; Mov34; 1.
DR Pfam: PF004392; Mov34; 1.
DR SMART: SM00232; JAR_MEN; 1.
DR CONFLICT 280 280
RV K -> R (IN REF. 2).
SQ SEQUENCE 291 AA; 33340 MW; 82D18B79D8EC5F72 CRC64;

Query Match 100.0%; Score 24; DB 1; Length 291;
Best local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
Db 280 KEELM 284
|||||

RESULT 13
ICE2_RAT STANDARD: PRT: 312 AA.
ID ICE2_RAT
AC P55215; Q35398;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

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15-JUN-2002 (Rel. 41, Last annotation update)  
 Caspase-2 precursor (EC 3.4.22.2) (CASP 2) (ICH 1 protease)  
 (Fragment).  
 CASP2 OR ICH1  
 Rattus norvegicus (Rat).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]  
 SOURCE OF 1-257 FROM N.A.  
 RP TISSUE=Ovary;  
 RC TISSUE=Kidney cortex;  
 RX MEDLINE=98191409; PubMed=950276;  
 RA Kauschal G.P., Singh A.B., Shan S.V.;  
 RT Identification of gene family of caspases in rat kidney and altered  
 PL expression in ischemia-reperfusion injury.\*;  
 PL Am J Physiol 274:F587-F595(1998)  
 [2]  
 RP SEQUENCE OF 131-312 FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=96042508; PubMed=7588240;  
 RA Flaws J.A., Kugu K., Tibbovich A.M., Desautels A., Lilly K.;  
 RA Hirshfield A.N., Lilly J.L.;  
 RT Interleukin-1 beta-converting enzyme-related proteases (IRPs) and  
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal  
 RT endonuclease activity from morphological apoptosis in granulosa cells  
 RT of the ovarian follicle.\*;  
 RL Endocrinology 136:5042-5053(1995)  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. MIGHT FUNCTION BY EITHER  
 CC ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING  
 CC PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY  
 CC SIMILARITY).  
 CC -1- PIM: THE MAJORITY PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT  
 CC THAT OF OTHER CASPASES (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN  
 CC  
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 CC  
 DR EMBL: AF025671; AA025671.1;  
 DR EMBL: U34684; AA025671.1;  
 DR HSP: P29466; LICE.  
 DR MEROPS: C14.006;  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002198; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00619; CARD; 1.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR SMART: SM00114; CARD; 1.  
 DR SMART: SM00115; CARD; 1.  
 DR PROSITE: PS02029; CARD; 1.  
 DR PROSITE: PS02028; CASPASE\_P20; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1  
 KW Hydrolyase, Thiol, Peptidase, Apoptosis, Cysteine, Zymogen.  
 FT NON\_TER 1 257  
 FT CHAIN <1 256  
 FT CASPASE-2 SUBUNIT P18 (BY SIMILARITY)  
 FT CHAIN 267 >312  
 FT CASPASE-2 SUBUNIT P13 (BY SIMILARITY).  
 FT CHAIN 281 >312  
 FT CASPASE-2 SUBUNIT P12 (BY SIMILARITY)  
 FT DOMAIN <1 55  
 FT CARD  
 FT ACT\_SITE 210 210  
 FT BY SIMILARITY.  
 FT ACT\_SITE 253 253  
 FT BY SIMILARITY.  
 FT NON\_TER 312 312  
 FT SEQUENCE 312 AA: 35070 MW: 31804746.21296646 Da  
 Query Match 100.0% Score 24. DB 1. Local 312;  
 Best Local Similarity 100.0% Prod. No. 1e-02;  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;  
 QY 1 KEELM 5  
 DB 283 KEELM 287  
 [1]  
 RESULT 14  
 C61A\_HUMAN  
 ID C61A\_HUMAN STANDARD: PRT: 316 AA.  
 AC P4746, Q9P127, Q16107,  
 DT 01 NOV 1995 (Rel. 32, Created)  
 DT 15 JUN 2002 (Rel. 41, Last sequence update)  
 DT 15 JUN 2002 (Rel. 41, Last annotation update)  
 DE C6.1A protein.  
 GN C6.1A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Placenta;  
 RX MEDLINE=91245099; PubMed=1301175;  
 RP Mott J.N., Levinson B., Taylor S., Shapiro A., Gitschler J.;  
 RA Kowalik S., Levinson B., Taylor S., Shapiro A., Gitschler J.;  
 RT Isolation and sequence of two genes associated with a CpG island 5'  
 RT of the factor VIII gene.\*;  
 PL Hum Mol Genet 1:179-186(1992)  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2). AND CHROMOSOMAL TRANSLOCATION.  
 RX MEDLINE=94067776; PubMed=8247530;  
 RA Fisch P., Forster A., Sherrington P., Dyer M.J.S., Rabbitts T.H.;  
 RT The chromosomal translocation t(X;14)(q28;q11) in T cell pro-  
 RT lymphocytic leukaemia breaks within one gene and activates another.\*;  
 RL Oncogene 8:3271-3276(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Lung;  
 RX Strausberg R.;  
 PL Submitted (APR-2001) to the EMBL/GenBank/DBS databases.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 and 2 (shown here); are  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal  
 CC muscle, kidney and pancreas.  
 CC -1- DISEASE: A form of pre-lymphocytic t-cell leukemia (T-PLL) is  
 CC characterized by a chromosomal translocation t(X;14)(q28;q11)  
 CC that involves C6.1A and T-cell receptor alpha chain (TCRA)  
 CC genes.  
 CC -1- SIMILARITY: BELONGS TO THE PSMD7/C6.1A FAMILY.  
 CC  
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 CC  
 DR EMBL: X64643; CAA45917.1;  
 DR EMBL: S68015; AA029005.2; ALL\_INIT.  
 DR EMBL: X602299; AA02999.1;  
 DR EMBL: RC000540; AA00540.1;  
 DR InterPro: IPR00555; Mov34  
 DR Pfam: PF01398; Mov34; 1.  
 DR ProDom: PD04402; Mov34; 1.  
 DR SMART: SM00232; JAB.MPN; 1.  
 KW Photo oncogene, Chromosomal translocation, Alternative splicing.  
 FT VERSITIC 184 208  
 FT MISSING (IN ISOFORM 1).  
 FT CONFLICT 225 225  
 FT G 35 W (IN REF. 2).  
 FT SEQUENCE 316 AA: 35072 MW: 52235861.4219664;

Query Match 100.0%; Score 24; DH 1; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 I I I I I  
 DB 305 KEELM 309

## RESULT 15

Y014\_METJA STANDARD; PRI: 316 AA.  
 AC Q60349;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein MJ0034.  
 GN MJ0034.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcales; Methanocaldococcus.  
 OX NCBI\_TaxID-2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE-9637799; PubMed-8688087;  
 RA Bult C.J., White O., Olsen G.T., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Goodbagon N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Utterback T.R., Kelley T.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M.,  
 RA Kleuk H.-P., Fraser C.M., Smith D.O., Woese C.R., Venter J.C.;  
 RF "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 RL Science 273:1058-1073(1996).

CC -!- SIMILARITY: BELONGS TO THE UPF0051 (YCF24) FAMILY.  
 CC -----  
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DR EMBL; U67462; AAB98015.1; -;  
 DR TIGR; MJ0034; -;  
 DR InterPro; IPR000825; UPF0051.  
 DR Pfam; PF01458; UPF0051; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 316 AA; 35021 MW; 3657AC25CHH473D1 CRC64;

Query Match 100.0%; Score 24; DH 1; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5  
 I I I I I  
 DB 4 KEELM 8

Search completed: January 16, 2003, 16:51:10  
 Job time : 8.28571 secs